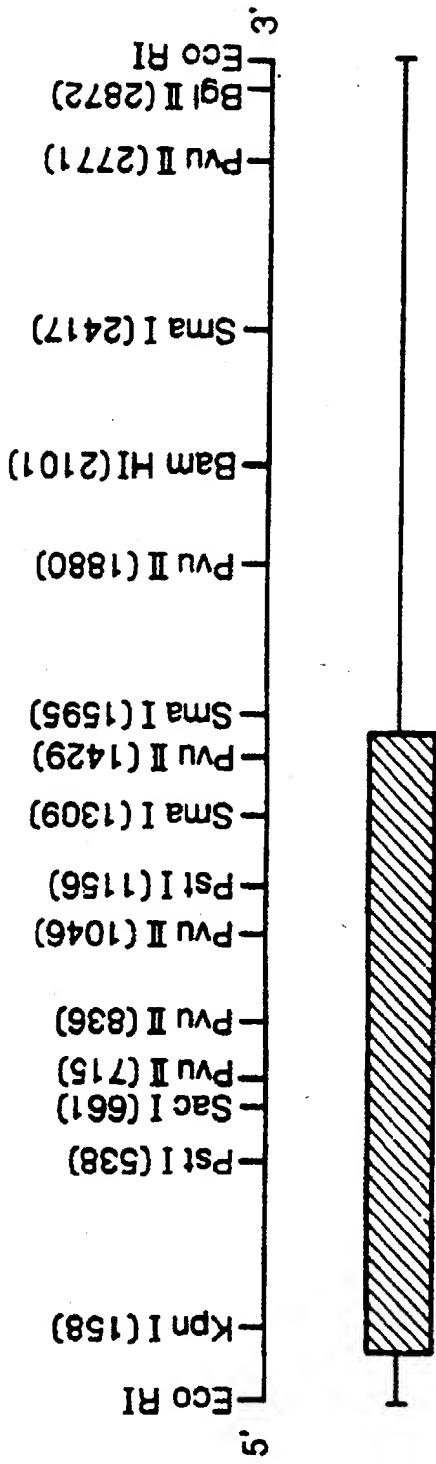


FIG. IA**FIG. IB-1**

1 GCCATCTGGCCAGGCCATGCCCGAGGGGGTGTGAAGGCCACAGGCCACTGCCAGACTGTCGCCTCCCTCTGACTG
 Met Ala Ser Alan Ser Ser Ser Pro Thr Phe Leu Gly Ile Gly His Leu Asn Glu Ile Tyr Pro Val Pro Arg Ile Tyr Ala Phe
 91 TGGCCGCTGGCATGGCCAGAACAGGAGCTCCTGCCGACACTGGGGACCTCAATGGGTACCCGGTACGCCCTACGCCCTC
 Phe Phe Pro Pro Met Leu Gly Ile Ser Pro Pro Gln Ile Thr Leu Gln Ile Ser Pro Val Ile Ser Gln Ile Tyr Ser Thr Pro
 TTCTCCCCCTATGCTGGTGGACTCTCCCGGCCAGGACCTCTCCAGCACCTCCAGTTCCAGTTAGTGQATATAGCACCCA
 Lys Phe Asp Thr Ile Glu Ile Ser Ser Ser Glu Ile Ile Val Pro Ser Pro Pro Ser Pro Pro Arg Ile Tyr Lys
 181 TCCCAGCACCATTGAGACCCAGGGAGGAGCTCTGAGAGATAGTGCCTAGCCAGCTCCCTACCCCTACCCGCACTACAG
 Ser Pro Ala Thr Ile Glu Thr Ile Ser Ser Ser Glu Ile Ile Val Pro Ser Pro Pro Ser Pro Pro Arg Ile Tyr Lys
 271 TCCCAGCACCATTGAGACCCAGGGAGGAGCTCTGAGAGATAGTGCCTAGCCAGCTCCCTACCCCTACCCGCACTACAG

FIG. IB-3

1171 E A L K 381 V R K R P S R 371 F P K A L M K 381 T D C R S
 GAGGCCGCTAAAGGTCTACGTGGGAACGGGAGCCAGCCAGGGAGC
 1181 I S A K 391 A E R V 1 / Thr Leu Ile Val Arg Pro Ser Arg Pro His
 Ile Ser Pro Ser Arg Pro Ser Arg Pro His
 1261 Ser Glu Gly Ile Asp Thr Leu Ser Gly Ile Val Arg Pro His
 ATAGGGCCAAGGGGGTGAAGGGGTGATGGAGATGGCTGAAGCTAACGCT
 1351 D S E G L 421 T L S G Q P G G 431 R D G G G L A P P 441 G S C S P
 Ser Glu Gly Ile Asp Thr Leu Ser Gly Ile Val Arg Pro His
 TAGAGGGCTGGACACTCTAGGGGAGACGGGAGCCGGGGTGGGGGG
 1441 S L S P 451 S A N P S R S R P O A L A T H I T S S P R O End
 Ser Leu Ser Pro Ser Ser Asn Pro Ser Ser Asn Pro Ser End
 AGCCCTAGCCCCAGTCACCAAGAAGCAGCCCCACTCCCCGTGACCCACAT
 1531 CGGCTTTCTGCCTTCTACCGACCATGTGACCCGCCACCAAGCCCCT
 1621 GGGGACGGGGAGGGAGGGAGGGAGCCACTCTGGACAGGGCCT
 1711 AGGCCGAGGCCAGGAACACTGAGTGAAGGCCCTGGTCTGGGT
 1801 CAGCTCACCAATCTTCATCACCAAGAACGCCAGGAACCTGGC
 1891 CTCAACCTCCCCCTGCCCTGGCTGACAGGGGGTGGGACAGGG
 1981 GGATTAAATTCTGCCTGGTTTATTTTATTTAATTTTTATTA
 2071 AAGGAATTGGCTGCTGTATGGGGGGAGCTGGATCCAGAGCT
 2161 TCTCCCTTCATGTCTCCCTGTGCCCTCCAGTTCCTCAAGCT
 2251 AAGGCCTGCCCTCCCTCCACTGGAGAAGGCCAGGCCCT
 2341 CCTGAAGGACAGGCTCTGGCCTGGCAGGTGCTGCCCTGGC
 2431 TCCCAAGACCTGGCTCTCGGAGGTGCTGCCCTGGCAGGT
 2521 GGGCCGAGCTGCCCTCACCCGGGCTCAAGGCCACAGGCC
 2611 ACACACACACACTGGACAGTAGATGGGGGAGACACACT
 2701 CACCCCCGGTGGCCCCCTCCCTACGGGGGGCTACGGGG
 2791 CCCCGACCTCTTCACCAAGGGGTTGGGGCCCTTCCCTGG
 2881 GATAAAGATAAAGITCTATTATCTAAAAA
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